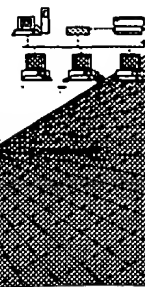


BEST AVAILABLE COPY

BIOTECHNOLOGY
SYSTEMS
BRANCH



0500

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/636,530

Source: OIPF

Date Processed by STIC: 8/17/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/636,530

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☒ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 08/17/2000
 PATENT APPLICATION: US/09/636,530 TIME: 10:08:21

Input Set : A:\CIP pharma Sequence Listing Ascii.txt
 Output Set: N:\CRF3\08162000\I636530.raw

Does Not Comply
 Corrected Diskette Needed

4 <110> APPLICANT: Cantor, Thomas L.
 6 <120> TITLE OF INVENTION: Parathyroid Hormone Antagonists or Modulators and Uses Therefor
 9 <140> CURRENT APPLICATION NUMBER: US/09/636,530
 9 <141> CURRENT FILING DATE: 2000-08-10
 0 <130> FILE REFERENCE:
 9 <160> NUMBER OF SEQ ID NOS: 5
 11 <170> SOFTWARE: Microsoft Word 2000 - ASCII format

OK
 WOK

*Suggestion: Consult
 new Sequence Rules*

ERRORED SEQUENCES

14 <210> SEQ ID NO: 1
 16 <211> LENGTH: 84 ~~{integer length}~~
 18 <212> TYPE: PRT
 20 <213> ORGANISM: human parathyroid hormone peptide fragment
 22 <400> SEQUENCE: 1
 24 Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu
 25 1 5 10 15
 27 Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp
 28 20 25 30
 30 Val His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp
 31 35 40 45
 33 Ala Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val
 34 50 55 60
 36 Glu Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val
 37 65 70 75
 E--> 39 Asn Val Leu Thyr Lys Ala Lys Ser Gln
 40 80
 43 <210> SEQ ID NO: 2
 45 <211> LENGTH: 83 ~~{integer length}~~
 47 <212> TYPE: PRT
 49 <213> ORGANISM: human parathyroid hormone peptide fragment
 51 <400> SEQUENCE: 2
 53 Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn
 54 1 5 10 15
 56 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
 57 20 25 30
 60 His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala
 61 35 40 45
 63 Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu
 64 50 55 60
 66 Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn
 67 65 70 75
 E--> 69 Val Leu Thyr Lys Ala Lys Ser Gln
 70 80
 73 <210> SEQ ID NO: 3
 75 <211> LENGTH: 51 ~~{integer length}~~

← delete globally - do not show template

*invalid - do not show modifications
 in the sequence itself.
 Explain in 22207-22237
 section*

RAW SEQUENCE LISTING DATE: 08/17/2000
 PATENT APPLICATION: US/09/636,530 TIME: 10:08:21

Input Set : A:\CIP pharma Sequence Listing Ascii.txt
 Output Set: N:\CRF3\08162000\I636530.raw

77 <212> TYPE: PRT
 79 <213> ORGANISM: human parathyroid hormone peptide fragment
 81 <400> SEQUENCE: 3
 83 Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly Ser
 E--> 84 1 5 10 15
 86 Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser His
 E--> 87 20 25 30
 89 Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn Val Leu
 E--> 90 35 40 45
 E--> 92 Thyr Lys Ala Lys Ser Gln
 E--> 93 50
 96 <210> SEQ ID NO: 4
 98 <211> LENGTH: 82 ~~[integer length]~~
 100 <212> TYPE: PRT
 102 <213> ORGANISM: human parathyroid hormone peptide fragment
 104 <400> SEQUENCE: 4
 106 Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn Ser
 107 1 5 10 15
 109 Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His
 110 20 25 30
 112 Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly
 113 35 40 45
 115 Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser
 116 50 55 60
 118 His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn Val
 119 65 70 75
 E--> 121 Leu Thyr Lys Ala Lys Ser Gln
 122 80
 126 <210> SEQ ID NO: 5
 128 <211> LENGTH: 57 ~~[integer length]~~
 130 <212> TYPE: PRT
 132 <213> ORGANISM: human parathyroid hormone peptide fragment
 134 <400> SEQUENCE: 5
 136 Leu Gln Asp Val His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala
 137 1 5 10 15
 139 Pro Arg Asp Ala Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn
 140 20 25 30
 142 Val Leu Val Glu Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys
 143 35 40 45
 E--> 145 Ala Asp Val Asn Val Leu Thyr Lys Ala Lys Ser Gln
 146 50 55

*misaligned amino acids -
 see item 4 on Enol
 summary sheet*

invalid

VERIFICATION SUMMARY DATE: 08/17/2000
PATENT APPLICATION: US/09/636,530 TIME: 10:08:22

Input Set : A:\CIP pharma Sequence Listing Ascii.txt
Output Set: N:\CRF3\08162000\I636530.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:39 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:39 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:69 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:69 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:84 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
M:332 Repeated in SeqNo=3
L:92 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:92 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:121 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:121 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:145 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:145 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1